

### **In the Specification**

Please replace the paragraph beginning on page 5 line 8 with the following amended paragraph:

Similarity analysis includes database search and alignment. Examples of public databases include the DNA Database of Japan (DDBJ)(~~http://www.~~ available on the worldwide web at: ddbj.nig.ac.jp/); Genebank (~~http://www.ncbi.nlm.nih.gov~~ available on the worldwide web at the NCBI website at: /web/Genbank/Index.html); and the European Molecular Biology Laboratory Nucleic Acid Sequence Database (EMBL) (~~http://www.~~ available on the worldwide web at: ebi.ac.uk/ebi\_docs/embl\_db.html). A number of different search algorithms have been developed, one example of which are the suite of programs referred to as BLAST programs. There are five implementations of BLAST, three designed for nucleotide sequences queries (BLASTN, BLASTX, and TBLASTX) and two designed for protein sequence queries (BLASTP and TBLASTN) (Coulson, *Trends in Biotechnology*, 12: 76-80 (1994); Birren, *et al.*, *Genome Analysis*, 1: 543-559 (1997)).

Please replace the paragraph beginning on page 27 line 22 with the following amended paragraph:

A PCR probe is a nucleic acid molecule capable of initiating a polymerase activity while in a double-stranded structure with another nucleic acid. Various methods for determining the structure of PCR probes and PCR techniques exist in the art. Computer generated searches using programs such as Primer3 (~~[[www-]]~~ available on the worldwide web at: genome.wi.mit.edu/cgi-bin/primer/primer3.cgi), STSPipeline (~~[[www-]]~~ available on the worldwide web at:

genome.wi.mit.edu/cgi-bin/www-STS\_Pipeline), or GeneUp (Pesole *et al.*, *BioTechniques* 25:112-123 (1998) the entirety of which is herein incorporated by reference), for example, can be used to identify potential PCR primers.